

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/038,895A

DATE: 04/03/2003 TIME: 12:06:46

Imput Set : E:\3379.1.ST25.txt

Output Set: N:\CRF4\04032003\J038895A.raw

```
3 <110> APPLICANT: Kulp, David C.
             Siani-Bose, Michael A.
             Williams, Alan J.
             Harmon, Cyrus L.
      - - - 12(c) TITLE GF INVENTION: Nucleic Acids Encoding G Proteins Coupled Receptors
     10 -1300- FILE REFERENCE: -379.1
     1. RIACH CURRENT ASPLICATION NUMBER: 10/038,895A
C--> 13 <141> CURRENT FILING DATE: 2003-03-25
     15 RINGS PRIOR APPLICATION NUMBER: US 60/244,082
     1: -:151: PELOF FILING DATE: 2000-10-26
     1- -:160: NUMBER OF SEQ ID NO3: 20:
     26 - 176 - SOFTWAFF: Patientin version 3.2
     n. ROLD SEQ ID NO: I
     0 - -0.1110 LENGTH: 274
     M4 -001A0- TYPE: FET
     Df HOTE: OFGANISM: Artificial Sequence
                                                                       ENTERED
       - CO. OF FEATURE:
     1 = -(MLE) OTHER INFORMATION: Synthetic Organism
     31 HOUGH FEATURE:
     F. Hill DE NAME/HEY: misc feature
     3 * *index LogATION: (186)...(186)
     54 GEORGE OTHER INFORMATION: Maa dan be any naturally occurring amino acid
     SA HILL OF FEATURE:
     37 -t., 13 NAME/HEY: misd feature
     From: 3F LOCATION: (146)..(146)
     39 0.3330 CTHEF INFCEMATION: Maa dan be any naturally occurring amino acid
     41 -4001 SEQUENCE: 1
     4. Len hen Ala Pro Thr Gly Ser Len Phe Arg Asr Cys Thr Gln Asp Gly
    44 1
                                             10
       Try Ser Glu Thr Phe Pro Arg Pro Ash Leu Ala Cys Gly Val Ash Val
                                         25
                                                             30
                    2 -
    11 Ast. Asp der Ser Act. Glu Lys Ang Ser Tyr Leu Leu Lys Leu Lys Val
                35
                                    40
                                                         45
     !! Mer Tyr Thr Val Gly Tyr Ser Ser Ser Leu Val Met Leu Leu Val Ala
          50
                                55
     for her. Gly lie Leb Cys Ala Phe Arg Arg Lou His Cys Thr Arg Ash Tyr
                            70
                                                 75
     65 Ile His Met His Lou Fhe Val Ser Phe Ile Leu Arg Ala Leu Ser Aun
                                                                 95
                        85
                                             90
     67 Pho Ile Lys Asp Ala Val Leu Phe Ser Ser Asp Asp Val Thr Tyr Cys
                                        105
                                                             110
                    100
    71 Asp Ala His Arg Gly Cys Lys Leu Val Met Val Leu Phe Xaa Tyr Cys
```

120

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```
75 Ile M t Ala A:n Tyr Ser Trp Leu Leu Val Slu Gly Ser Thr Phe Thr
     7.. 1.0
                                135
                                                     140
     70 His Kaa Lea Ala lle Ser Phe Phe Ser Glu Arg Lys Tyr Leu Gln Gly
                                                 155
                             150
     Fr Phot Val Ala Phot Gly Trp Gly Ser Pro Ala Ile Phe Val Ala Leu Trp
                                                                  175
                        165
                                             170
        Ala lle Ala Arq His Phe Leu Glu Asp Val Gly Cys Trp Asp Ile Ash
                                                              190
                                         135
     91 Ali Ann Ala Ser Ilo Trp Trp Ile Ile Arg Sly Pro Val Ile Leu Ser
                                     200
     98 Ile Beu Ash Phe Ile Leu Phe Ile Ash Ile Leu Arg Ile Leu Met Arg
                                                     220
            ..10
                                 215
     90 Lyv Dea Ang Thr Olm Gla Thr Ang Gly Ash Gla Val Ser His Tyr Lys
     1 .0 ...5
                                                  235
                             230
     1 & Ary Deu Ala Ary Ser Thr Leu Leu Leu Ile Pro Leu Phe Gly Ile His
                         2.45
                                             250
     10 / Tyr lle Mal Phe Ara Phe Ser Pro Glu Asp Ala Met Glu Ile Gln Leu
                                          265
     10%
                     260
     111 Phe Phe
     115 % 10 / SEQ ID NO: 3
     116 -0111 - LENGTH: 381
     117 HLID - TYPE: DNA
     118 - 0.113 - OFCANISM: Artificial Sequence
     1.0 -120 - FEATURE:
     1/1 -(103- OTHER INFORMATION: Synthetic Organism
     123 - 4400 - SEQUENCE: 2
                                                                                 60
     114 efectionsead compagnite estightnega aactgeacae agganggeng gheagaaace
                                                                                120
     116 theocoasgo ofwatetiqo ofgtggggtt aatgfgaacg actoffccaa ogagaagogg
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     1.6 castoctace tgetgaaget gaaagteatg tacacegtgg getacagete etcectggte
     1\% algebraicing togeocity categorists gettle-egga gyetecacty cactegoade
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     1%; tabatobaca tigoacciqti ogiqtoctic atoottogiq cociqtocaa citcatcaag
                                                                                360
     1\% gauge-graph telephone agangangte acchaetgeg angeceacag ggegggenge
                                                                                 331
     1:6 augustgatea tagtactatt d
     1:9 0.10 - SEQ 15 NO: 3
     140 -1.11 - LENGTH: 447
     141 - DIE: DNA
     14. HOLER OF GANISM: Artificial Sequence
     144 ANTON FEATURE:
     145 CLLA: OTHER INFORMATION: Synthetic Organism
     14% H. O. FEATUFE:
     149 H. H: NAME/KEY: misc feature
     150 HLIDE LOCATION: (58)...(58)
     151 HILLS OTHER INFORMATION: n is a, c, g, or t
     15% RADIO SEQUENCE: 3
W--> 154 tactgcatca tggccaacta ctcctggctg ctggtggaag gctctacctt cacacatntc
                                                                                120
     15) of eghcatic contestes tigaaagaaag taceteeagg gattigtigge atteggatigg
     1:W gattetecag coattitigt tgettigtgg getattgeca gaeactitet ggaagatgit
                                                                                180
                                                                                240
     100 gdqtgctggg acatcaatgc caacgcatcc atctggtgga tcattcgtgg tcctgtgatc
```

162 crotocator tgattaatti catcottito ataaacatto taaqaatoot gatgagaaaa

300

RAW SEQUENCE LISTING

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DATE: 04/03/2003

Input Set : E:\3379.1.ST25.txt

Output Set: N:\CRF4\04032003\J038895A.raw

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164 ottagaacco aagaaacaag aggaaatgaa gtcagccatt ataagcgcct ggccaggtcc
                                                                                                                                                     360
         1) 6 actoroctyc tgatececet etitygeate cactacateg tettegeett etececagag
                                                                                                                                                     411
                                                                                                                                                     4.0
         1.8 gacquitatgg adatocaget gtttttt
         101 <210 - SEQ II NO: 4
         17% < ::11 + LENGTH: 828
         173 KM11 - TYPE: DNA
         174 KM1 + ORGANISM: Artificial Sequence
         196 CLOG - FEATURE:
         177 CLESS OTHER INFORMATION: Synthetic Organism
         180 HIGG: FEATURE:
         1-1 -0.01 - MAME/KEY: mist_feature
         1-. -0.000 - 1000ATION: (439)...(439)
         1:3 days OTHER IMPORMATION: n is a, c, g, or t
         185 8400 8 SEQUENCE: 4
         180 chiminggeat concaditto offigitocga aactgbasac aggatggotg gtoagaaacc
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         141 which octog tomocostogy datectotyt gotttoogga ggotocacty castogbaac
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         194 tack bears typhacetytt egtyteette attettegty ebetyteess ettestbass.
         1 W quarrangings testificate agaignings accidentaged algebrased ggoggguings.
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         1 w garps gatea togatgetgtt etactgeate atggecaact actectgget getggt@gaa.
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W--> 200 ggctctacct tcacacatnt cctcgccatc tccttcttct ctgaaagaaa gtacctccag
         Dual that the top cantograte gegether bear good titting tigettigte gestatiges.
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         1600 Atoms togig giodigigat obtotobato otgatiaatt toatobttit bataaabatt.
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         III qforrogoet terecodaga ggaegetatg gagatebage tgtttttt
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         215 8210 8 SEQ ID NO: 5
         . 14 -0000 - DEMGTH: 320
         , 17 \pm, 1, \pm TYPE: PET
         218 -218 - ORGANISM: Artificial Sequence
         \mathbb{M} \cap \{0, 1, 0\} \in \mathsf{FEATURE}:
         ... 1 -0.7 - OTHER INFORMATION: Synthetic Organism
         11.7 4440 - SEQUENCH: 5
         ... 5 Pro Thr The I.e Lea Phe Ser Phe Gln Pro Gly Asp Lys Arg Thr Lys
                                                                                     10
         ... Her lie Cys Val Tyr Trp Glu Gly Ser Glu Gly Gly His Trp Ser Thr
                                                                             25
                                     2.1
         . - Go. Gly Cys Ser H.s Val His Ser Ash Gly Ser Tyr Thr Lys Cys Lys
                                                                      4 ()
         . Which the His Lou Ser Ser Phe Ala Val Leu Val Ala Leu Ala Pro Lys
         ...38
                                                             5,5
                                                                                                    60
         .41 App Pro Val Lea Thr Val Ile Thr Gin Val Gly Lea Thr Ile Ser Lea
         . 4.. 6°
                                                      7 Ô
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                 Lou Cys Leu Phe Lou Ala Ile Leu Thr Phe Leu Lou Cys Arg Pro Ile
                               8.
                                                                                     90
         149 Gin Asn Thr Ser Thr Ser Leu His Leu Glu Leu Ser Leu Cys Leu Phe
                                       100
                                                                              105
                                                                                                                    110
```

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TIME: 12:06:46

Input Set : E:\3379.1.ST25.txt

Output Set: N:\CRF4\04032003\J038895A.raw

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157	Leu	-	Ser	Lie	11e			Leu	Leu	His	Phe		Туг	Leu	Ala	Jys	
		130					131					140					
. 61	Phe	Thr	Trp	Met	Leu	Leu	G. :	317	Leu	His	Leu	Pn⊕	L⊕u	Thr	Val	Ang	
	145					150					155					; ti]	
266	$A^{\omega} \Pi$	Lea	Lys	Val	Ala	Ash	T - r	Thr	Ser	Thr	Gly	Arq	Prie	Lys	Lys	Arg	
, titi					165					170					: 7.5		
_ 6.3	Phe	Met	Tyr	Pro	V.i l	Gly	$T \cdot r$	Gly	Ile	Pro	Alā	V-a l	Ile	I1e	Ala	7.1	
70			•	180		1	•	•	185					190			
	Ser	Ala	T1e		Glv	Pro	G.r.	Asn		Glv	'I'h r	Phe	Thr	His	Cys	Trp	
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. 4	173	, =:		H y	Leu	Glγ	Paris		M⊕t	Val	Glu	GLG		GLY	Lys	l'itr	
14			277.5					230					285				
€97	110	GLY	S-1	11€	$I l \oplus$	Ala	Гуг	Ser	Phe	Thr	Ile	I l.+∋	Asn	Thr	Le u	3.5	
2110		<u>. 90</u>					295					300					
30:1	31.y	Val	Leu	Lega	Phe	Val.	Vıl	His	Cys	Leu	Leu	Asn	Arg	Gln	Val	Arg	
200.0	19:11 Ep					310					315					3.20	
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Output Set: N:\CRF4\04032003\J038895A.raw

346	6 paggt aagg															969	
3.1 +	• :::10> SEQ IE NO: 7																
351	- 3.1115 LENGTH: 217																
35:	CHRISTER TYPE: FWT																
3141	+0:13: ORGANISM: Artificial Sequence																
	HAMACON FEATURE:																
3:	<pre>% (COST) CTHER INFORMATION: Synthetic Organism % (400) SEQUENCE: 7</pre>																
			_														
354	(11 r.	Hils	3⊕r	$\tau^{r, L}$		Vā l	His	Asp	Ľ•ŝ.7		Leu	Asp	Val	Ile		Trp	
3.67					Č,					10				_	15		
	V.: l	$G1_{Y}^{*}$	Ile		Leu	Ser	Leu	Val	Суз	L⊕u	Leu	Ile	CAs		Phe	Thr	
				200					2.5			_		30			
	Phe	$C\Sigma \varepsilon$		F11.5	Arg	Gly	Leu		30r	Asp	Arg	Asr.		11€	Hls	LYS	
360			3.5					40		_ ,			4.5	,	* 3		
			Cys	Πē	Ser	ù⊜'ù		Val	Ala	Glu	Leu		Phe	Leu	11.6	G.L.Y	
37.		200				1	55		~	D)	1	6(n l	7.1.	T	•	
		As fi	Arg	Th.r	Asp		F.r.o	Alā	Суз	Ala		Pr.e	Ala	Ala	ьец		
- E		4		F-1	-	7 C	n 1	Б:	(TC)	(T)	75 M	151	T			80	
	His	Pr.∈	E'frei	t'llus:		Ala	ALā	Phe	Thr		Met	Præ	ЫUU	גוגנו	-95 -913	√ < 1 1	
321	., .	7			66		3.1 - 3	21	• 7 - 1	90 25	Cla	٦	(21)	ui.a		A room	
	J. I.	1/8/1	1771		ME: U	LÆ1.1	V (d.1	3 ! U	Val. 105	Fire	GLU	5U1	ما 1.5	110	Ser	Arg	
	*	,	271] HQ 54 -	111	1.0	57 - 1	71,7	Tyr	21	M +-	Dw.s.	315		T1a	17 : 1	
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				1 .	Tla		Aem	Va l	I læ	Prie		Glv	Ll∈	Alā	Leu		
400			272	•	1.65					170		1			175	•	
		Mert	F¹hi∈.	Hile.		Thi	Ala	He	Leu		Pro	Glu	Ser	Gly	Cys	Leu	
4:-4	,	• • • • •		1 × 6					183	1				190	•		
	ASO	Asn	Ile	LWS	Leu	Lys	He	Asn	Ile	Pro	Ile	Ile	Lys	Ser	Ile	Tyr	
4:1	•		195	•				200					205				
411	110	Tyr	Mest	Tyr	He	Cys	Met	Sys	Val								
41.		.10		•		-	215										
411	-1.10	S SI	EÇ II) <u>10</u>	5												
41	.:::	11. [.]	ENGTI	∃: 65	57												
417	-:::	: T	YEE:	$\mathbb{D}\mathbb{H}$													
41.5	•	50 - QI	RCAN:	13M:	Arti	ifia	ial S	Беди€	ende								
4. 1	·:: (July E'I	5,A,']''[.'}	E.E.:													
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																ctttat	300
434	a'ca	atgot	-dd .	iggad	ggttt	it to	gagaç	gtgaa	a Cat	itcad	gta	ggaa	aatad	out :	.tat(stggtc	360

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 04/03/2003 PATENT APPLICATION: US/10/038,895A

TIME: 12:06:47

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 126,146

Seq#:3; N Pos. 58 Seq#:4; N Pos. 439 Seq#:19; Xaa Pos. 370 VERIFICATION SUMMARY

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L:13 M:271 C: Current Filing Date difters, Replaced Current Filing Date

L:71 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:112

M:341 Repeated in SeqNo=1

L:154 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0 L:200 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:420 L:1587 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:368